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(71) Applicant (for all designated States except US): SMITHKLINE BEECHAM LABORATORIES PHARMACEUTIQUES [FR/FR]; 6, esplanade Charles de Gaulle, F-92731 Nanterre Cedex (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): BERREBI-BERTRAND, Isabelle, Therese [FR/FR]; (FR). BRIL, Antoine, Michel, Alain [FR/FR]; (FR). CALMELS, Thierry, Paul, Gerard [FR/FR]; (FR). FAIVRE, Jean-François, Simon, Pierre [FR/FR]; (FR). KRIEF, Stéphane, Clément [FR/FR]; (FR). ROBERT, Philippe, Laurent [FR/FR]; (FR). SOUCHET, Michel, Louis [FR/FR]; SmithKline Beecham Laboratoires Pharmaceutiques, 4, rue du Chesnay Beauregard, Boîte postale 58, F-35762 Saint Gregoire (FR).		
(54) Title: ADENOSINE NUCLEOTIDE TRANSLOCATOR		
(57) Abstract Adenine nucleotide translocator (ANT4) polypeptides and polynucleotides and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing ANT4 polypeptides and polynucleotides in therapy, and diagnostic assays for such.		

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ADENOSINE NUCLEOTIDE TRANSLOCATOR

Field of the Invention

5 This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in therapy and in identifying compounds which may be agonists, antagonists and /or inhibitors which are potentially useful in therapy, and to production of such polypeptides and polynucleotides.

Background of the Invention

10 The drug discovery process is currently undergoing a fundamental revolution as it embraces 'functional genomics', that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superceding earlier approaches based on 'positional cloning'. A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the
15 responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

20 The ADP/ATP translocator, or adenine nucleotide translocator (ANT), is the most abundant mitochondrial protein. In its functional state, ANT is a homodimer of 30-kD subunits embedded asymmetrically in the inner mitochondrial membrane. The dimer forms a gated pore through which ATP is moved from the matrix into the cytoplasm. Three distinct human ANT cDNAs have been cloned so far: ANT1, ANT2, and ANT3.

25

Summary of the Invention

The present invention relates to ANT4, in particular ANT4 polypeptides and ANT4 polynucleotides, recombinant materials and methods for their production. In another aspect, the invention relates to methods for using such polypeptides and polynucleotides, including the
30 treatment of congestive heart failure, ischaemic heart disease, cardiac arrhythmias, diastolic or systolic dysfunction, hypertrophic cardiomyopathy or stroke, hereinafter referred to as "the Diseases", amongst others. In a further aspect, the invention relates to methods for identifying agonists and antagonists/inhibitors using the materials provided by the invention, and treating conditions associated with ANT4 imbalance with the identified compounds. In a still further

aspect, the invention relates to diagnostic assays for detecting diseases associated with inappropriate ANT4 activity or levels.

Description of the Invention

5 In a first aspect, the present invention relates to ANT4 polypeptides. Such peptides include isolated polypeptides comprising an amino acid sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:2 over the entire length of SEQ ID NO:2. Such polypeptides include those comprising the amino acid of
10 SEQ ID NO:2.

Further peptides of the present invention include isolated polypeptides in which the amino acid sequence has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO:2 over the entire length of SEQ ID NO:2.
15 Such polypeptides include the polypeptide of SEQ ID NO:2.

Further peptides of the present invention include isolated polypeptides encoded by a polynucleotide comprising the sequence contained in SEQ ID NO:1.

Polypeptides of the present invention are believed to be members of the calcium-sensitive adenine nucleotide translocator family of polypeptides. They are therefore of interest because when
20 the contractile activity of the heart is stopped by cardiac arrest or ventricular fibrillation, about 60-70% of the oxygen uptake ceases, showing that most of the high-energy phosphate production by oxidative phosphorylation is directed toward contractile activity. Because the ANT determines the rate of ADP/ATP flux between the mitochondrion and the cytosol, it is a logical candidate for regulator of cellular dependence on oxidative energy metabolism. Muscular
25 contraction and relaxation are directly regulated by both energy and calcium fluxes in the cytoplasm. Importantly, we have cloned a novel calcium-sensitive adenine nucleotide translocator. This novel calcium-sensitive adenine nucleotide translocator may be instrumental in the regulation of energy fluxes by calcium, thus of muscle contractile function. These properties are hereinafter referred to as "ANT4 activity" or "ANT4 polypeptide activity" or "biological
30 activity of ANT4". Also included amongst these activities are antigenic and immunogenic activities of said ANT4 polypeptides, in particular the antigenic and immunogenic activities of the polypeptide of SEQ ID NO:2. Preferably, a polypeptide of the present invention exhibits at least one biological activity of ANT4.

The polypeptides of the present invention may be in the form of the "mature" protein or

may be a part of a larger protein such as a precursor or fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification such as multiple histidine residues, or an additional sequence for stability during recombinant production.

5 The present invention also include variants of the aforementioned polypeptides, that is polypeptides that vary from the referents by conservative amino acid substitutions, whereby a residue is substituted by another with like characteristics. Typical such substitutions are among Ala, Val, Leu and Ile; among Ser and Thr; among the acidic residues Asp and Glu; among Asn and Gln; and among the basic residues Lys and Arg; or aromatic residues Phe and Tyr. Particularly
10 preferred are variants in which several, 5-10, 1-5, 1-3, 1-2 or 1 amino acids are substituted, deleted, or added in any combination.

 Polypeptides of the present invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of
15 these methods. Means for preparing such polypeptides are well understood in the art.

 In a further aspect, the present invention relates to ANT4 polynucleotides. Such polynucleotides include isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, to the amino acid sequence of SEQ
20 ID NO:2, over the entire length of SEQ ID NO:2. In this regard, polypeptides which have at least 97% identity are highly preferred, whilst those with at least 98-99% identity are more highly preferred, and those with at least 99% identity are most highly preferred. Such polynucleotides include a polynucleotide comprising the nucleotide sequence contained in SEQ ID NO:1 encoding the polypeptide of SEQ ID NO:2.

25 Further polynucleotides of the present invention include isolated polynucleotides comprising a nucleotide sequence that has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, to a nucleotide sequence encoding a polypeptide of SEQ ID NO:2, over the entire coding region. In this regard, polynucleotides which have at least 97% identity are highly preferred, whilst those with at least 98-
30 99% identity are more highly preferred, and those with at least 99% identity are most highly preferred.

 Further polynucleotides of the present invention include isolated polynucleotides comprising a nucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, to SEQ

ID NO:1 over the entire length of SEQ ID NO:1. In this regard, polynucleotides which have at least 97% identity are highly preferred, whilst those with at least 98-99% identity are more highly preferred, and those with at least 99% identity are most highly preferred. Such polynucleotides include a polynucleotide comprising the polynucleotide of SEQ ID NO:1 as well as the

5 polynucleotide of SEQ ID NO:1.

The invention also provides polynucleotides which are complementary to all the above described polynucleotides.

The nucleotide sequence of SEQ ID NO:1 is a cDNA sequence and comprises a polypeptide encoding sequence (nucleotide 12 to 2048) encoding a polypeptide of 678 amino acids, 10 the polypeptide of SEQ ID NO:2. The nucleotide sequence encoding the polypeptide of SEQ ID NO:2 may be identical to the polypeptide encoding sequence contained in SEQ ID NO:1 or it may be a sequence other than the one contained in SEQ ID NO:1, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:2. The polypeptide of the SEQ ID NO:2 is structurally related to other proteins of the calcium- 15 sensitive adenine nucleotide translocator family, having homology and/or structural similarity with ADP, ATP carrier proteins (Wilson, R et al, Nature 368 (6466), 32-38 (1994).

Preferred polypeptides and polynucleotides of the present invention are expected to have, *inter alia*, similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention 20 have at least one ANT4 activity.

The present invention also relates to partial or other polynucleotide and polypeptide sequences which were first identified prior to the determination of the corresponding full length sequences of SEQ ID NO:1 and SEQ ID NO:2.

Accordingly, in a further aspect, the present invention provides for an isolated 25 polynucleotide comprising:

- (a) a nucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% identity to SEQ ID NO:3 over the entire length of SEQ ID NO:3;
- (b) a nucleotide sequence which has at least 70% identity, preferably at least 80% identity, more 30 preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% identity, to SEQ ID NO:3 over the entire length of SEQ ID NO:3;
- (c) the polynucleotide of SEQ ID NO:3; or
- (d) a nucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95%

identity, even more preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO:4, over the entire length of SEQ ID NO:4; as well as the polynucleotide of SEQ ID NO:3.

The present invention further provides for a polypeptide which:

- 5 (a) comprises an amino acid sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:4 over the entire length of SEQ ID NO:4;
- (b) has an amino acid sequence which is at least 70% identity, preferably at least 80% identity, 10 more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO:4 over the entire length of SEQ ID NO:4;
- (c) comprises the amino acid of SEQ ID NO:4; and
- (d) is the polypeptide of SEQ ID NO:4;
- 15 as well as polypeptides encoded by a polynucleotide comprising the sequence contained in SEQ ID NO:3.

The nucleotide sequence of SEQ ID NO:3 and the peptide sequence encoded thereby are derived from EST (Expressed Sequence Tag) sequences. It is recognised by those skilled in the art that there will inevitably be some nucleotide sequence reading errors in EST sequences (see 20 Adams, M.D. *et al*, Nature 377 (supp) 3, 1995). Accordingly, the nucleotide sequence of SEQ ID NO:3 and the peptide sequence encoded therefrom are therefore subject to the same inherent limitations in sequence accuracy. Furthermore, the peptide sequence encoded by SEQ ID NO:3 comprises a region of identity or close homology and/or close structural similarity (for example a conservative amino acid difference) with the closest homologous or structurally similar protein.

25 Polynucleotides of the present invention may be obtained, using standard cloning and screening techniques, from a cDNA library derived from mRNA in cells of human heart, brain, uterus, mammary gland, lung, prostate, kidney, trachea, stomach, liver, placenta, testis, small intestine, spinal cord, ovary, spleen, pancreas, thymus, aorta, eye, leukocyte, skeletal muscle, adrenal, adipose, lymph node, colon, thyroid, bone marrow, bladder, salivary gland or appendix 30 using the expressed sequence tag (EST) analysis (Adams, M.D., *et al*. *Science* (1991) 252:1651-1656; Adams, M.D. *et al*, *Nature*, (1992) 355:632-634; Adams, M.D., *et al*, *Nature* (1995) 377 Supp:3-174). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself; or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence which facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, *Proc Natl Acad Sci USA* (1989) 86:821-824, or is an HA tag. The polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Further embodiments of the present invention include polynucleotides encoding polypeptide variants which comprise the amino acid sequence of SEQ ID NO:2 and in which several, for instance from 5 to 10, 1 to 5, 1 to 3, 1 to 2 or 1, amino acid residues are substituted, deleted or added, in any combination.

Polynucleotides which are identical or sufficiently identical to a nucleotide sequence contained in SEQ ID NO:1, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction, to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding paralogs from human sources and orthologs and paralogs from species other than human) that have a high sequence similarity to SEQ ID NO:1. Typically these nucleotide sequences are 70% identical, preferably 80% identical, more preferably 90% identical, most preferably 95% identical to that of the referent. The probes or primers will generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50 nucleotides. Particularly preferred probes will have between 30 and 50 nucleotides. Particularly preferred primers will have between 20 and 25 nucleotides.

A polynucleotide encoding a polypeptide of the present invention, including homologs from species other than human, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO: 1 or a fragment thereof; and isolating full-length cDNA and genomic clones containing said polynucleotide sequence. Such hybridization techniques are well known to the skilled artisan. Preferred stringent hybridization conditions include overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10 % dextran sulfate.

and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0.1x SSC at about 65°C. Thus the present invention also includes polynucleotides obtainable by screening an appropriate library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO:1 or a fragment thereof.

5 The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide is short at the 5' end of the cDNA. This is a consequence of reverse transcriptase, an enzyme with inherently low 'processivity' (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during 1st
10 strand cDNA synthesis.

 There are several methods available and well known to those skilled in the art to obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., PNAS USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon™ technology
15 (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon™ technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the 'missing' 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated
20 using 'nested' primers, that is, primers designed to anneal within the amplified product (typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analysed by DNA sequencing and a full-length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate
25 full-length PCR using the new sequence information for the design of the 5' primer.

 Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems which comprise a polynucleotide or polynucleotides of the present invention, to host cells which are genetically
30 engineered with such expression systems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

 For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Introduction of

polynucleotides into host cells can be effected by methods described in many standard laboratory manuals, such as Davis et al., Basic Methods in Molecular Biology (1986) and Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989). Preferred such methods include, for instance, calcium phosphate
5 transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as *streptococci*, *staphylococci*, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and
10 *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, episomal and virus-derived systems, e.g., vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements,
15 from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector which is able to maintain, propagate or
20 express a polynucleotide to produce a polypeptide in a host may be used. The appropriate nucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL* (*supra*). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen
25 of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the
30 medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography,

hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during
5 intracellular synthesis, isolation and or purification.

This invention also relates to the use of polynucleotides of the present invention as diagnostic reagents. Detection of a mutated form of the gene characterised by the polynucleotide of SEQ ID NO:1 which is associated with a dysfunction will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-
10 expression, over-expression or altered spatial or temporal expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification techniques prior
15 to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to labeled ANT4 nucleotide sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by
20 alterations in electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (see, e.g., Myers *et al.*, *Science* (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (see Cotton *et al.*, *Proc Natl Acad Sci USA* (1985) 85: 4397-4401). In another embodiment, an array of oligonucleotides probes comprising ANT4
25 nucleotide sequence or fragments thereof can be constructed to conduct efficient screening of e.g., genetic mutations. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability (see for example: M.Chee *et al.*, *Science*, Vol 274, pp 610-613 (1996)).

30 The diagnostic assays offer a process for diagnosing or determining a susceptibility to the Diseases through detection of mutation in the ANT4 gene by the methods described. In addition, such diseases may be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of polypeptide or mRNA. Decreased or increased expression can be measured at the RNA level using any of the methods well known in

the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art.

- 5 Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagnostic kit which comprises:

- (a) a polynucleotide of the present invention, preferably the nucleotide sequence of SEQ ID NO: 1, or a fragment thereof ;
(b) a nucleotide sequence complementary to that of (a);
(c) a polypeptide of the present invention, preferably the polypeptide of SEQ ID NO:2 or a fragment thereof; or
(d) an antibody to a polypeptide of the present invention, preferably to the polypeptide of SEQ ID NO:2.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, particularly congestive heart failure, ischaemic heart disease, cardiac arrhythmias, diastolic or systolic dysfunction, hypertrophic cardiomyopathy or stroke, amongst others.

- 20 The nucleotide sequences of the present invention are also valuable for chromosome localisation. The sequence is specifically targeted to, and can hybridize with, a particular location on an individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data.
25 Such data are found in, for example, V. McKusick, Mendelian Inheritance in Man (available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes). The gene of the present invention maps to human chromosome 2q31-q32.

30 The differences in the cDNA or genomic sequence between affected and unaffected individuals can also be determined. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

The nucleotide sequences of the present invention are also valuable for tissue localisation. Such techniques allow the determination of expression patterns of the ANT4 polypeptides in tissues by detection of the mRNAs that encode them. These techniques include in situ hybridization techniques and nucleotide amplification techniques, for example PCR. Such techniques are well known in the art. Results from these studies provide an indication of the normal functions of the polypeptides in the organism. In addition, comparative studies of the normal expression pattern of ANT4 mRNAs with that of mRNAs encoded by a ANT4 gene provide valuable insights into the role of mutant ANT4 polypeptides, or that of inappropriate expression of normal ANT4 polypeptides, in disease. Such inappropriate expression may be of a temporal, spatial or simply quantitative nature.

The polypeptides of the invention or their fragments or analogs thereof, or cells expressing them, can also be used as immunogens to produce antibodies immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, analogs or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., *Nature* (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, pp. 77-96, Alan R. Liss, Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography.

Antibodies against polypeptides of the present invention may also be employed to treat the Diseases, amongst others.

In a further aspect, the present invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various

subclasses (IgG, IgM, IgA, IgE). Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa. Furthermore, this invention relates
5 to processes for the preparation of these fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and therapy. A further aspect of the invention also relates to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos. WO94/29458 and WO94/22914.

Another aspect of the invention relates to a method for inducing an immunological
10 response in a mammal which comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response to protect said animal from the Diseases hereinbefore mentioned, amongst others. Yet another aspect of the invention relates to a method of inducing immunological response in a mammal which
15 comprises, delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce such an immunological response to produce antibody to protect said animal from diseases.

A further aspect of the invention relates to an immunological/vaccine formulation (composition) which, when introduced into a mammalian host, induces an immunological response in that mammal to a polypeptide of the present invention wherein the composition
20 comprises a polypeptide or polynucleotide of the present invention. The vaccine formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous, intramuscular, intravenous, or intradermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats
25 and solutes which render the formulation isotonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include
30 adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Polypeptides of the present invention are responsible for one or more biological functions, including one or more disease states, in particular the Diseases hereinbefore mentioned. It is

therefore desirous to devise screening methods to identify compounds which stimulate or which inhibit the function of the polypeptide. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those which stimulate or which inhibit the function of the polypeptide. In general, agonists or antagonists may be employed for
5 therapeutic and prophylactic purposes for such Diseases as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. Such agonists, antagonists or inhibitors so-identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; or may be structural or functional mimetics thereof (see Coligan *et al.*, *Current*
10 *Protocols in Immunology* 1(2):Chapter 5 (1991)).

The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve competition with a labeled competitor. Further, these
15 screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Constitutively active polypeptides may be employed in screening
20 methods for inverse agonists or inhibitors, in the absence of an agonist or inhibitor, by testing whether the candidate compound results in inhibition of activation of the polypeptide. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring ANT4 activity in the mixture, and comparing the ANT4 activity of the mixture to a standard. Fusion
25 proteins, such as those made from Fc portion and ANT4 polypeptide, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, *J Mol Recognition*, 8:52-58 (1995); and K. Johanson *et al.*, *J Biol Chem*, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the polypeptide of the present
30 invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents which may inhibit or enhance the production of polypeptide (also called

antagonist or agonist, respectively) from suitably manipulated cells or tissues.

The polypeptide may be used to identify membrane bound or soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance, ^{125}I), chemically modified (for instance, biotinylated), or fused to a peptide sequence suitable for detection or purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supernatants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide which compete with the binding of the polypeptide to its receptors, if any. Standard methods for conducting such assays are well understood in the art.

Examples of potential polypeptide antagonists include antibodies or, in some cases, oligonucleotides or proteins which are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, e.g., a fragment of the ligands, substrates, receptors, enzymes, etc.; or small molecules which bind to the polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Thus, in another aspect, the present invention relates to a screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes, etc. for polypeptides of the present invention; or compounds which decrease or enhance the production of such polypeptides, which comprises:

- (a) a polypeptide of the present invention;
 - (b) a recombinant cell expressing a polypeptide of the present invention;
 - (c) a cell membrane expressing a polypeptide of the present invention; or
 - (d) antibody to a polypeptide of the present invention;
- which polypeptide is preferably that of SEQ ID NO:2.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

It will be readily appreciated by the skilled artisan that a polypeptide of the present invention may also be used in a method for the structure-based design of an agonist, antagonist or inhibitor of the polypeptide, by:

- (a) determining in the first instance the three-dimensional structure of the polypeptide;
- (b) deducing the three-dimensional structure for the likely reactive or binding site(s) of an agonist, antagonist or inhibitor;
- (c) synthesizing candidate compounds that are predicted to bind to or react with the deduced

binding or reactive site; and

(d) testing whether the candidate compounds are indeed agonists, antagonists or inhibitors.

It will be further appreciated that this will normally be an iterative process.

5 In a further aspect, the present invention provides methods of treating abnormal conditions such as, for instance, congestive heart failure, ischaemic heart disease, cardiac arrhythmias, diastolic or systolic dysfunction, hypertrophic cardiomyopathy or stroke, related to either an excess of, or an under-expression of, ANT4 polypeptide activity.

10 If the activity of the polypeptide is in excess, several approaches are available. One approach comprises administering to a subject in need thereof an inhibitor compound (antagonist) as hereinabove described, optionally in combination with a pharmaceutically acceptable carrier, in an amount effective to inhibit the function of the polypeptide, such as, for example, by blocking the binding of ligands, substrates, receptors, enzymes, etc., or by inhibiting a second signal, and thereby alleviating the abnormal condition. In another approach, soluble forms of the polypeptides still capable of binding the ligand, substrate, enzymes, receptors, etc. in competition with endogenous
15 polypeptide may be administered. Typical examples of such competitors include fragments of the ANT4 polypeptide.

In still another approach, expression of the gene encoding endogenous ANT4 polypeptide can be inhibited using expression blocking techniques. Known such techniques involve the use of antisense sequences, either internally generated or externally administered (see, for example,
20 O'Connor, *J Neurochem* (1991) 56:560 in *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Alternatively, oligonucleotides which form triple helices ("triplexes") with the gene can be supplied (see, for example, Lee *et al.*, *Nucleic Acids Res* (1979) 6:3073; Cooney *et al.*, *Science* (1988) 241:456; Dervan *et al.*, *Science* (1991) 251:1360). These oligomers can be administered *per se* or the relevant oligomers can be
25 expressed *in vivo*. Synthetic antisense or triplex oligonucleotides may comprise modified bases or modified backbones. Examples of the latter include methylphosphonate, phosphorothioate or peptide nucleic acid backbones. Such backbones are incorporated in the antisense or triplex oligonucleotide in order to provide protection from degradation by nucleases and are well known in the art. Antisense and triplex molecules synthesised with these or other modified backbones
30 also form part of the present invention.

In addition, expression of the ANT4 polypeptide may be prevented by using ribozymes specific to the ANT4 mRNA sequence. Ribozymes are catalytically active RNAs that can be natural or synthetic (see for example Usman, N, *et al.*, *Curr. Opin. Struct. Biol* (1996) 6(4), 527-33.) Synthetic ribozymes can be designed to specifically cleave ANT4 mRNAs at selected

positions thereby preventing translation of the ANT4 mRNAs into functional polypeptide.

Ribozymes may be synthesised with a natural ribose phosphate backbone and natural bases, as normally found in RNA molecules. Alternatively the ribozymes may be synthesised with non-natural backbones to provide protection from ribonuclease degradation, for example, 2'-O-methyl
5 RNA, and may contain modified bases.

For treating abnormal conditions related to an under-expression of ANT4 and its activity, several approaches are also available. One approach comprises administering to a subject a therapeutically effective amount of a compound which activates a polypeptide of the present invention, i.e., an agonist as described above, in combination with a pharmaceutically acceptable
10 carrier, to thereby alleviate the abnormal condition. Alternatively, gene therapy may be employed to effect the endogenous production of ANT4 by the relevant cells in the subject. For example, a polynucleotide of the invention may be engineered for expression in a replication defective retroviral vector, as discussed above. The retroviral expression construct may then be isolated and introduced into a packaging cell transduced with a retroviral plasmid vector containing RNA
15 encoding a polypeptide of the present invention such that the packaging cell now produces infectious viral particles containing the gene of interest. These producer cells may be administered to a subject for engineering cells *in vivo* and expression of the polypeptide *in vivo*. For an overview of gene therapy, see Chapter 20, *Gene Therapy and other Molecular Genetic-based Therapeutic Approaches*, (and references cited therein) in Human Molecular Genetics, T Strachan and A P
20 Read, BIOS Scientific Publishers Ltd (1996). Another approach is to administer a therapeutic amount of a polypeptide of the present invention in combination with a suitable pharmaceutical carrier.

In a further aspect, the present invention provides for pharmaceutical compositions comprising a therapeutically effective amount of a polypeptide, such as the soluble form of a
25 polypeptide of the present invention, agonist/antagonist peptide or small molecule compound, in combination with a pharmaceutically acceptable carrier or excipient. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention.
30 Polypeptides and other compounds of the present invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

The composition will be adapted to the route of administration, for instance by a systemic or an oral route. Preferred forms of systemic administration include injection, typically by intravenous injection. Other injection routes, such as subcutaneous, intramuscular, or

intraperitoneal, can be used. Alternative means for systemic administration include transmucosal and transdermal administration using penetrants such as bile salts or fusidic acids or other detergents. In addition, if a polypeptide or other compounds of the present invention can be formulated in an enteric or an encapsulated formulation, oral administration may also be possible.

- 5 Administration of these compounds may also be topical and/or localized, in the form of salves, pastes, gels, and the like.

The dosage range required depends on the choice of peptide or other compounds of the present invention, the route of administration, the nature of the formulation, the nature of the subject's condition, and the judgment of the attending practitioner. Suitable dosages, however, are in the range of 0.1-100 $\mu\text{g/kg}$ of subject. Wide variations in the needed dosage, however, are to be expected in view of the variety of compounds available and the differing efficiencies of various routes of administration. For example, oral administration would be expected to require higher dosages than administration by intravenous injection. Variations in these dosage levels can be adjusted using standard empirical routines for optimization, as is well understood in the art.

- 15 Polypeptides used in treatment can also be generated endogenously in the subject, in treatment modalities often referred to as "gene therapy" as described above. Thus, for example, cells from a subject may be engineered with a polynucleotide, such as a DNA or RNA, to encode a polypeptide *ex vivo*, and for example, by the use of a retroviral plasmid vector. The cells are then introduced into the subject.

- 20 Polynucleotide and polypeptide sequences form a valuable information resource with which to identify further sequences of similar homology. This is most easily facilitated by storing the sequence in a computer readable medium and then using the stored data to search a sequence database using well known searching tools, such those in the GCG and Lasergene software packages. Accordingly, in a further aspect, the present invention provides for a computer readable medium having stored thereon a polynucleotide comprising the sequence of SEQ ID NO:1 and/or
- 25 a polypeptide sequence encoded thereby.

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

- 30 "Antibodies" as used herein includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, including the products of an Fab or other immunoglobulin expression library.

"Isolated" means altered "by the hand of man" from the natural state. If an "isolated" composition or substance occurs in nature, it has been changed or removed from its original

environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

"Polynucleotide" generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotides" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, biotinylation, covalent attachment of flavin.

covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., Post-translational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", *Meth Enzymol* (1990) 182:626-646 and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", *Ann NY Acad Sci* (1992) 663:48-62).

"Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

"Identity" reflects a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, determined by comparing the sequences. In general, identity refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of the two polynucleotide or two polypeptide sequences, respectively, over the length of the sequences

being compared. For sequences where there is not an exact correspondence, a "% identity" may be determined. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in either one or both sequences, to enhance the degree of alignment. A % identity may be determined over the whole
5 length of each of the sequences being compared (so-called global alignment), which is particularly suitable for sequences of the same or very similar length, or over shorter, defined lengths (so-called local alignment), which is more suitable for sequences of unequal length.

"Similarity" is a further, more sophisticated measure of the relationship between two polypeptide sequences. In general, "similarity" means a comparison between the amino acids of
10 two polypeptide chains, on a residue by residue basis, taking into account not only exact correspondences between a between pairs of residues, one from each of the sequences being compared (as for identity) but also, where there is not an exact correspondence, whether, on an evolutionary basis, one residue is a likely substitute for the other. This likelihood has an associated 'score' from which the "% similarity" of the two sequences can then be determined.

15 Methods for comparing the identity and similarity of two or more sequences are well known in the art. Thus for instance, programs available in the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J et al, Nucleic Acids Res, 12, 387-395, 1984, available from Genetics Computer Group, Madison, Wisconsin, USA), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity
20 and the % similarity between two polypeptide sequences. BESTFIT uses the "local homology" algorithm of Smith and Waterman (J Mol Biol, 147,195-197, 1981, Advances in Applied Mathematics, 2, 482-489, 1981) and finds the best single region of similarity between two sequences. BESTFIT is more suited to comparing two polynucleotide or two polypeptide sequences which are dissimilar in length, the program assuming that the shorter sequence
25 represents a portion of the longer. In comparison, GAP aligns two sequences, finding a "maximum similarity", according to the algorithm of Needleman and Wunsch (J Mol Biol, 48, 443-453, 1970). GAP is more suited to comparing sequences which are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters "Gap Weight" and "Length Weight" used in each program are 50 and 3, for polynucleotide sequences
30 and 12 and 4 for polypeptide sequences, respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned.

Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, J Mol Biol, 215, 403-410, 1990, Altschul S F et al, Nucleic Acids Res., 25:389-3402, 1997, available from

the National Center for Biotechnology Information (NCBI), Bethesda, Maryland, USA and accessible through the home page of the NCBI at www.ncbi.nlm.nih.gov) and FASTA (Pearson W R, Methods in Enzymology, 183, 63-99, 1990; Pearson W R and Lipman D J, Proc Nat Acad Sci USA, 85, 2444-2448, 1988, available as part of the Wisconsin Sequence Analysis Package).

5 Preferably, the BLOSUM62 amino acid substitution matrix (Henikoff S and Henikoff J G, Proc. Nat. Acad Sci. USA, 89, 10915-10919, 1992) is used in polypeptide sequence comparisons including where nucleotide sequences are first translated into amino acid sequences before comparison.

 Preferably, the program BESTFIT is used to determine the % identity of a query
10 polynucleotide or a polypeptide sequence with respect to a polynucleotide or a polypeptide sequence of the present invention, the query and the reference sequence being optimally aligned and the parameters of the program set at the default value, as hereinbefore described.

 "Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a reference sequence. Such
15 relatedness may be quantified by determining the degree of identity and/or similarity between the two sequences as hereinbefore defined. Falling within this generic term are the terms "ortholog", and "paralog". "Ortholog" refers to polynucleotides/genes or polypeptide which are homologs via speciation, that is closely related and assumed to have common descent based on structural and functional considerations. "Paralog" refers to polynucleotides/genes or polypeptide which are
20 homologs via gene duplication for instance, duplicated variants within a genome.

 "Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion
25 protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, e.g., EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified.

30 All publications, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference as if each individual publication were specifically and individually indicated to be incorporated by reference herein as though fully set forth.

SEQUENCE INFORMATION

SEQ ID NO:1

COGAGCAAGCATGGCGGTCAAGGTGCAGACAACTAAGCGAGGGGATCCTCATGAGTTAAGAAACATATTTCTACAGTAT
 GCCAGTACTGAGGTTGATGGAGAGCGTTACATGACCCAGAACACTTTGTTGAGCGCTATCTTGGAGTGTATATGATCC
 5 AAATAGTAACCCAAAGATCGTGAGCTCTTGCCAGGAGTAGCTGATCAAAACAAGGATGGGTTGATCTCCTATCAAGAGT
 TTTTGGCATTGTAATCTGTTTTATGTGCTCCAGATTCCATGTTCATAGTGGCTTTCCAGTTGTTTGACAAGAGTGGAAT
 GGAGAGGTGACATTTGAAAATGTCAAAGAAATTTTGGACAGACTATTATTATCATCATATCCCTTTAACTGGGATTG
 TGAATTTATCCGACTGCATTTTGGCATAAACGGAAGAAGCATCTTAACTACACAGAATTACGCGAGTTTCTCCAGGAGC
 TGAATTTGGAAATGCAAGACAAGCCTTTGCACTCAAAGACAAAAGCAAAAGTGGCATGATTTCTGGTCTGGATTTGAGT
 10 GACATCATGGTTACCATTAGATCTCACATGCTTACTCCTTTGTGGAGGAGAACTTAGTTTCAAGAGCTGGAGGAAGTAT
 CTCAACAGGTTAGCTTCTCCTACTTCAATGCATTTAACTCGTTACTGAATAACATGGAGCTTGTTCTGAAGATATATA
 GCACTCTAGCTGGCAAGGAAAGATGTTGAAGTCAAAAGGAGGAATTTGCCAGAGTGCCATACGCTATGGACAAGTCA
 ACCACTAGAAATTGATATTCTATATCAGCTTGAGACTTATATATGCTTCAAGGGCGCTTGACTTTGGCAGATATTGA
 GAGAATAGCCCCATTGGCTGAGGGGGCCTTACCTTACAACCTGGCAGAACTTCAGAGACAGCAGTCTCCTGGGTTAGGCA
 15 GGCTATCTGGCTCCAGATTGCCAGAGTCTGCTTACAGATTCACTCTGGGCTCAGTTGCTGGAGCTGTGGGAGCCATGCA
 GTGTATCCTATAGATCTGGTGAAGACCCGAATGCAAAACAGCGTGGCTCTGGCTCTGTTGTTGGGGAGCTAATGTACAA
 AAACAGCTTTGACTGTTTTAAGAAAGTCTGCGTTATGAGGGCTCTTTGGACTCTACAGGGGTCTGATACCACAACTTA
 TAGGGGTGCTCCAGAAAAGGCCATTAACTGACTGTTAATGATTTTGTTCGGGACAAATTTACAGAAAGAGATGGCTCT
 GTTCCAATTCCAGCAGAAGTTCTTGCTGGAGGCTGTGCTGGAGGCTCTCAGGTCAATTTTACCAACCCATTGGAGATAGT
 20 GAAGATTCTGCAAGTAGCTGGAGAGATCAACACGGGACCCAGAGTCAGCGCCCTGAATGTGCTCCGGGACTTGGGAA
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 CATTGCAAACTACTTCTGGCTGATGAAATGGACAGTGGGAGGTTTAAATCTTCTGCACTGGAGCCATGGCAGGTGT
 CCCAGCTGCATCTCTGGTGAACCCCTGCTGATGTATCAAGACAAGACTGCAGGTGGCTGCCGCGCTGGCCAGACGACAT
 ACAGTGGTGTCTGCACTGTTTCAAGGAAGATTCTCCGGGAAGAGGGCCCTCAGCATTTTGGAAAGGACTGCAGCTCGA
 25 GTGTTTGGATCCTCTCCCCAGTTTGGTGTACCTTGGTCACTTATGAACCTCTCCAGCGGTGGTTTTACATTGATTTTGG
 AGGCCTCAAAACCGCTGGTTCAGAACCAACACCTAAGTCAAGCATTGCAGACCTTCTCCTGCCAACCTGATCACATCG
 GTGGATACAGACTCGCCACAGCCAAGTTTGAGGCATCGAAAACAAATTTGGCCTTTATCTCCGAAATTTAAGTCTCCT
 AGTGTTGCTGTGGTTGAGCCAAAGGCAGCAGTGGCAGCCACTCAGTGATGAGACAACTGTTGAGTGTGGCAAAATGGCGC
 CTTGAAGAAAGAGGCCTAGGAGAGCAGCCCTGTAAATGTATCCAGTCAGCTGCATGGTACTGACTGAGCTGAGGAGTCAAA
 30 CTCTTTCTGTATGACATATACATATACCTGTTTATAAAATAATCATTGCCCAGGGAAAAACCAACGCTGTTTC
 AAGCTTTAGTCTTATGTGTTGAAATGTTTTGTAAACCTTGGCATGAATTAGTGTTCTAGACTCTGCTTGCAAGCTTG
 CACTTACAGTGATTGTACATATTGTACATCTTGTACAGAGACATCTTGGCACTCATCCCAACAAATCACATTTGTAGA
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 TTAAATGTGTGTAGACCTCCTCTGTTCAATCAAAAGCATTTCTAGGCAGCTCCTCGCTGTGAGTGTGCATATGG
 AAACAGGGACATCTCCATCACTACTGGCTTGTGTTTTGCTTCTTTGACACAGTAAGGCAAAAGGCCAAGCTTTCAAAAGA
 GTAAAGGATACCTTACAATTTCCCTCATATGGATATGATTCCAGTCAAAATAAAATGCACCAAAATGTTAAAAAA
 40 AAAAAAAAAAAAA

SEQ ID NO:2

MAVKVQTTK RGD PHEL RNI FLQYA STEVDGE RYMT PED FVQ RYLG LYN DP NSNPKIVQLLAGVADQTKDGLI SYQEFLAF
 E SVLCAPD SMFIVAFQLEDK SGNGEVTFENVKEIFGQTI IHHHIP FNWD CEFI RLHFWHNKKHLNYTEETQFLQELQLE
 HARQAFALKDK SK SGMISGLDFSDIMVTI RSHMLTPFEENLV SAAGGST SHQV SF SYFNAFNSLLNNMELV RKIYSTLA
 5 GT RKDVEVTKEEFAQSAI RYQVTPLEID ILYQLADLYNA SGR LTLADIE RIAP LAEGALPYNLAELQ RQQSPGLG RPIW
 LQIAE SAY RFTLG SVAGAVGAT AVYPID LVKT RMQNRG SG SVVGELMYKNSFD CFKKVL RYEGFFGLY RGLIPQLIGVA
 PEKAIKLT VND FV ROKFT RFDG SVPLP AEVL AGG CAGG SQVI FT NP LEIVKI RLQVAGEITTGP RV SALNVL RDLGIFGL
 YKGAKACFL RPIF SAIYFPVYAHCKLLADENGHVGLNLLAAGAMAGVPAASLVTP ADVIKT RLQVAA RAGQTTY SGV
 ID CF RKIL REEGP SAFWKGTAA RVF RS SPQFGVT LVT YELLO RWFYID FGGLKPA G SEPTPK SRIADLPPANPDHIGGYR
 10 LATAT FAGIENKFGLYLPKFK SP SVAVVQPKAAVAATQ

SEQ ID NO:3

AAGCTTGGCA CGAGGCCT CGTGCCAAGGAGAACTT AGTTT CAGCAGCTGGAGGAAGTAT CT CACACCAGGTT AGCTT CT C
 CTACTT CAATG CATTAACT CGTTACTGAATAACATGGAGCTTGTT CGTAAGATAT ATAGCACTCTAGCTGGCACAAGGA
 AAGATGTTGAAGT CACAAAGGAGGAATTTGCCAGAGTGCCATACGCTATGGACAAGT CACACCACTAGAAATTGATATT
 15 CTATAT CAGCTTG CAGACTTAT ATATGCTT CAGGGCGCTTGACTTTGGCAGATATTGAGAGAATAGCCCCATTGGCTGA
 GGGGGCCTTACCTTACAACTGGCAGAACTT CAGAGACAGCAGTCT CCTGGGTAGGCAGGCCTATCTGGCTCCAGATTG
 CCGAGTCTGCTTACAGATTCACTCTGGGCTCAGTTGCTGGAGCTGTGGGAGCCA CTG CAGTGTAT CCTATAGATCTGGT
 GAAGACCCGAATGCAAAACCAAGCCTGGCTCTGGCTCTGTTGTTGGGGAGCTAAATGTACAAAAACAGCTTTGACTGTTTT
 AAGAAAGTYTTGCTTATGAGGGCTTCTTTGGACTCTACAGGGGTCTGATACCACAACTATAGGGGTTKCTCCAGAAA
 20 AGGCCATTAACTGACTCTTAAATGATTTTGT CGGGA CAAATTTACCAGAAGAGATGGCTCTGTTCCACTTCCAGCAGAA
 GTTCTTGCTGGAGGCTGTGCTGGAGGCTCTCAGGT CATTTTTACCAACCCATTGGAGATAGTGAAGATTCTGCTGCAAGT
 AGCTGGAGAGATCA CCA CGGGACCCAGAGT CAGCGCCCTGAATGTGCT CCGGGACTTGGGAATTTTTGGTCTGTAT AAGG
 GTGCCAAAGCGTGTTCCTCGAGACATTCCCTCTCTGCAATCTATTTTCTGTTTATGCTCATTGCAAACTACTCTG
 GCTGATGAAATGGACAACGTGGGAGGTTTAAATCTTCTG CAGCTGGTAGCATGGCAGGTGTCCAGCTGCATCTCTG
 25 GTGgAMCCCYGCTGATGT CATCAAR GACAA R GACTG CAGgTKG STGCCGCGCTGGCCAGACGACATACAGTGGTGT CAT
 CGACTGTTT CAGGAAGATTCTCCGGGAAGAAGGSCCTCAGCattttggaAGGGA CTK CAGCTCGAGTGTTCGATCCT
 CTCCCCAGTTTGGTGTTACCTTGGTCACTTATGAACCTCTCCAGCGGTGGTTTTACATTGATTTTGGAGgCCTCAAAACC
 GCTGGTTtCAGAACCAACACCTAAGTCA CGCATTG CAGACCTTCTCTGCCAACCTGatCACATCGGTGGATACAGAC
 TCGCCACAGCCACGTTtGCAGGCATCGAAAA CAAATTTGGCCTTTATCTCCGAAATTTAAGTCTCCTAGTGTGCTGTG
 30 GTT CAGCCAAAGG CAGCAGTGGCAGCCA CT CAGTGATGAGACAACTGTTGgAGTGTGGCAAAATGGCGCCTTGAAGAAAG
 AGGCCTAGGAGAGCAGCCCTGT AATGTATCCAGT CAGCTGCATGGTACTGACTGAGCTGAGGAGTCAAACTCTTCTTCT
 GTATGACATATACATATACCTGTTTATAAATAATCATTTGCCAGGGAAAAACCAACGCTGTTTCAAGCTTTAGTC
 TTATGTGTTGAAATGTTTTGT AAGCCTTGGCATGAATTAGTGTTCTAGACTCTGCTTGCA CAGCTTGCACTTACAGTG
 ATTGTACATATTGTACATCTTTGTACAGAGACATCTTGGCACCTCATCCCAACAAATCATTGTTAGAAATGT AATGCG
 35 GTTCTGAGTGGCTTGAAATGTACAGAATGTTTTGAAAGTGTGTTTATTAAGAATCACACAAAAATAATGTATTAAAATTA
 AATTCACTCTCTATTGGTGACTTATGGAATAAAGCATCAATATTGGATGTATTTAATTCTAGTTKGTGTTTCCATTCT
 GGAATAAAAGGTATTTGCTGATAAAAGGCATACGAGACATAGTGCTGCTACCACTGAATAAGTGATACCTTGGGAAAG
 ATGCGATGCCAGTGGATGCCAGAGGACAGGCTAATGACTGTGTGCTGATGTGkTTTCCATTtGTATTTAATGTGTG
 TAGACCTCTCTGTTCATCAATCAAAAAGCATTTCCTAGGHAGCTCCTCGCCTGT CAGTGTGCATATGGAAA CAGGGAC
 40 ATCTCCAYCATTACTGGCTT AGTTKK SYTTY CYTTTGACACAGT AAGGCAAAGGCCAAGCTTTCAAAAGAGTAAAGGATA

CTTT CACAATTT CCCTT CAT ATGGAT ATGATT CCAGT CAAAAAT AAAAT GCAC CCAAATGT AAAAAAAAAA

SEQ ID NO:4

MELV RKIY SLAGT RKDVEVTKEEFAQ SAI RYQVTP LEID ILYQLADLYN ASG RLT LADIE RIAP LAEGALPYN LAELQ
5 RQQ SPGLGRPIWLQIAE SAY RFT LGLSCW SCG SHCSV SY RSGEDP NAKPAWLWLCCWGAK CTKTALTVLKKXCVMRAFFG
LYRGLIPQLIGVXPEKAIKLTVNDFV RDKET RFDG SVP LP AEVL AGG CAGG SQVI FT NP LEIVKI RLQVAGEITTGP RVS
ALNVL RDLGIFGLYKGAKACFL RDI PF SAIYFPVYAHCKLLADENGQ RGRFK SSCSWXPWQV SQLHLWWXP ADVIKDKD
CRXXPALARRHTVV SSTVSG RFS REEGPQHFGKGLQLECFDPLP SLVLPW SLMNFS SGGFT LILEASNPLV SEPTPK SRI
ADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSP SVAVVQPKAAVAATQ

10

SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION
- (i) APPLICANT: SmithKline Beecham Laboratoires Pharmaceutiques
- 10 (ii) TITLE OF THE INVENTION: Novel Compounds
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: SmithKline Beecham, Corporate Intellectual
Property
(B) STREET: Two New Horizons Court
(C) CITY: Brentford
(D) STATE: Middlesex
20 (E) COUNTRY: UK
(F) ZIP: TW8 9EP
- (v) COMPUTER READABLE FORM:
- 25 (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- 30 (2) INFORMATION FOR SEQ ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2973 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

	COGAGCACAG	CATGGGGT C	AAGGTGCAGA	CAACTAAGCG	AGGGGAT CCT	CATGAGTTAA	60
	GAAACATATT	TCTACAGTAT	GCCAGTACTG	AGGTTGATGG	AGAGCGTTAC	ATGACCCACG	120
	AAGACTTTGT	TCAGCGCTAT	CTTGGACTGT	ATAATGATCC	AAATAGTAAC	CCAAAGATCG	180
5	TGCAGCTCTT	GGCAGGAGTA	GCTGAT CAAA	CCAAGGATGG	GTTGAT CT CC	TATCAAGAGT	240
	TTTTGGCATT	TGAATCTGTT	TTATGTGCTC	CAGATTCCAT	GTTCATAGTG	GCTTTCCAGT	300
	TGTTTGACAA	GAGTGGAAAT	GGAGAGGTGA	CATTTGAAAA	TGTCAAAGAA	ATTTTTGGAC	360
	AGACTATTAT	T CATCATCAT	ATCCCTTTTA	ACTGGGATTG	TGAATTTATC	CGACTGCATT	420
	TTTGGCATAA	COGGAAGAAG	CATCTTAAC	ACACAGAATT	CACGAGTTT	CTCCAGGAGC	480
10	TGCAATTGGA	ACATGCAAGA	CAAGCCTTTG	CACCAAAGA	CAAAAGCAAA	AGTGGCATGA	540
	TTTCTGGTCT	GGATTT CAGT	GACATCATGG	TTACCATTAG	ATCTCACATG	CTTACTCCTT	600
	TTGTGGAGGA	GAACCTAGTT	TCAGCAGCTG	GAGGAAGTAT	CTCACACCAG	GTTAGCTTCT	660
	CCTACTTCAA	TGCATTTAAC	TCGTTACTGA	ATAACATGGA	GCTTGTT CGT	AAGATATATA	720
	GCACTCTAGC	TGGCACAAGG	AAAGATGTTG	AAGTCAAAA	GGAGGAATTT	GCCCAGAGTG	780
15	CCATACGCTA	TGGACAAGTC	ACACCACTAG	AAATTGATAT	TCTATATCAG	CTTGCCAGACT	840
	TATATAATGC	TTCAGGGGCG	TTGACTTTGG	CAGATATTGA	GAGAATAGCC	CCATTGGCTG	900
	AGGGGGCCTT	ACCTTACAAC	CTGGCAGAAC	TTCAGAGACA	GCAGTCTCCT	GGGTTAGGCA	960
	GGCCTATCTG	GCTCCAGATT	GCCGAGTCTG	CTTACAGATT	CACTCTGGGC	TCAGTTGCTG	1020
	GAGCTGTGGG	AGCCACTGCA	GTGTATCCTA	TAGATCTGGT	GAAGACCCGA	ATGCAAAACC	1080
20	AGCGTGGCTC	TGGCTCTGTT	GTTGGGGAGC	TAATGTACAA	AAACAGCTTT	GACTGTTTTA	1140
	AGAAAGTCTT	GCGTTATGAG	GGCTTCTTTG	GACTCTACAG	GGGTCTGATA	CCACAACCTA	1200
	TAGGGGTTGC	TCAGAAAAG	GCCATTAAAC	TGACTGTAA	TGATTTTGT	CGGGACAAAT	1260
	TTACCAGAAG	AGATGGCTCT	GTTCCACTTC	CAGCAGAAGT	TCTTGCTGGA	GGCTGTGCTG	1320
	GAGGCTCTCA	GGTCATTTTT	ACCAACCCAT	TGGAGATAGT	GAAGATT CGT	CTGCAAGTAG	1380
25	CTGGAGAGAT	CACCAAGGGA	CCCAGAGTCA	GCGCCCTGAA	TGTGCTCCGG	GACTTGGGAA	1440
	TTTTTGGTCT	GTATAAGGGT	GCCAAAGCGT	GTTTCTCCG	AGACATTCCC	TTCTCTGCAA	1500
	TCTATTTTCC	TGTTTATGCT	CATTGCAAAC	TACTTCTGGC	TGATGAAAAT	GGACACGTGG	1560
	GAGGTTTAAA	TCTTCTTGCA	GCTGGAGCCA	TGGCAGGTGT	CCCAGCTGCA	TCTCTGGTGA	1620
	CCCCCTGCTGA	TGT CATCAAG	ACAAGACTGC	AGGTGGCTGC	CCGCGCTGGC	CAGACGACAT	1680
30	ACAGTGGTGT	CATCGACTGT	TTCAGGAAGA	TTCTCCGGGA	AGAAGGGCCC	TCAGCATTTT	1740
	GGAAAGGGAC	TGCAGCTCGA	GTGTTTGGAT	CCTCTCCCCA	GTTTGGTGT	ACCTTGGTCA	1800
	CTTATGAACT	TCTCCAGCGG	TGGTTTTACA	TTGATTTTGG	AGGCCTCAAA	CCCGCTGGTT	1860
	CAGAACCAAC	ACCTAAGTCA	CGCATTGCAG	ACCTTCTCC	TGCCAACCTT	GATCACATCG	1920
	GTGGATACAG	ACTCGCCACA	GCCAOGTTTG	CAGGCATCGA	AAACAAATTT	GGCCTTTATC	1980
35	TCCCGAAATT	TAAGTCTCCT	AGTGTGCTG	TGGTTCAGCC	AAAGGCAGCA	GTGGCAGCCA	2040
	CTCAGTGATG	AGACAACGT	TGAGTGTGGC	AAAATGGCGC	CTTGAAGAAA	GAGGCCTAGG	2100
	AGAGCAGCCC	TGTAATGTAT	CCAGTCAGCT	GCATGCTACT	GACTGAGCTG	AGGAGTCAAA	2160
	CTCTTCTTT	TGTATGACAT	ATACATATAC	TTGTTTATAA	AATAATCATT	TGCCCAGGGA	2220
	AAAAACCACA	ACGCTGTTTC	AAGCTTATGT	CTTATGTGTT	GAAATGTTTT	TGTAAGCCTT	2280
40	GGCATGAATT	AGTGTTCTAG	ACTCTGCTTT	GCACAGCTTG	CACCTACAGT	GATTGTACAT	2340
	ATTGTACATC	TTTGTACAGA	GACATCTTGG	CACCTCATCC	CAACAAATCA	CATTTGTAGA	2400

AATGTAATGC GGTTCGAGT GGCTTGAAAT GTACAGAATG TTTTGAAAGT GTTTTATTAA 2460
 GAATCACACA AAAATAAATG TATTAATAAT TAAATTCATT CTCTATTGG TGACTTATGG 2520
 AAATAAAGCA TCAATATTGG ATGTATTAA TTCCTAGTTT GTTTTCCATT CTGGAATAAA 2580
 AAGGTATTTG CTGATAAAAG GCATAACGAG ACATAGTGCT GCTACCACTG AATAAGTGAT 2640
 5 ACTTTGGGAA AGATGCATGC CAGTGGATGC CAGAGGACCA GGCTAATGAC TTGTGTGTGC 2700
 TGATGTGTTT CCATTTGTAT TTAATGTGTG TAGACCCTCC TCTGTT CAT C AATCAAAAAG 2760
 CATTTCCTAG GCAGCTCCTC GCCTGT CAGT GTGCATATGG AAACAGGGAC ATCTCCATCA 2820
 TTACTGGCCT AGTTTTGCTT TCCTTTGACA CAGTAAGGCA AAGGCCAAGC TTTCAAAAGA 2880
 GTAAAGGATA CTTTCACAAT TTCCCTCAT ATGGATATGA TTCCAGTCAA AAATAAATG 2940
 10 CACACCAAAA TGTTAAAAA AAAAAAAAAA AAA 2973

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 678 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

25 Met Ala Val Lys Val Gln Thr Thr Lys Arg Gly Asp Pro His Glu Leu
 1 5 10 15
 Arg Asn Ile Phe Leu Gln Tyr Ala Ser Thr Glu Val Asp Gly Glu Arg
 20 25 30
 Tyr Met Thr Pro Glu Asp Phe Val Gln Arg Tyr Leu Gly Leu Tyr Asn
 35 40 45
 30 Asp Pro Asn Ser Asn Pro Lys Ile Val Gln Leu Leu Ala Gly Val Ala
 50 55 60
 Asp Gln Thr Lys Asp Gly Leu Ile Ser Tyr Gln Glu Phe Leu Ala Phe
 65 70 75 80
 Glu Ser Val Leu Cys Ala Pro Asp Ser Met Phe Ile Val Ala Phe Gln
 35 85 90 95
 Leu Phe Asp Lys Ser Gly Asn Gly Glu Val Thr Phe Glu Asn Val Lys
 100 105 110
 Glu Ile Phe Gly Gln Thr Ile Ile His His His Ile Pro Phe Asn Trp
 115 120 125
 40 Asp Cys Glu Phe Ile Arg Leu His Phe Trp His Asn Arg Lys Lys His
 130 135 140

28

465 470 475 480
 Tyr Lys Gly Ala Lys Ala Cys Phe Leu Arg Asp Ile Pro Phe Ser Ala
 485 490 495
 Ile Tyr Phe Pro Val Tyr Ala His Cys Lys Leu Leu Leu Ala Asp Glu
 5 500 505 510
 Asn Gly His Val Gly Gly Leu Asn Leu Leu Ala Ala Gly Ala Met Ala
 515 520 525
 Gly Val Pro Ala Ala Ser Leu Val Thr Pro Ala Asp Val Ile Lys Thr
 530 535 540
 10 Arg Leu Gln Val Ala Ala Arg Ala Gly Gln Thr Thr Tyr Ser Gly Val
 545 550 555 560
 Ile Asp Cys Phe Arg Lys Ile Leu Arg Glu Glu Gly Pro Ser Ala Phe
 565 570 575
 Trp Lys Gly Thr Ala Ala Arg Val Phe Arg Ser Ser Pro Gln Phe Gly
 15 580 585 590
 Val Thr Leu Val Thr Tyr Glu Leu Leu Gln Arg Trp Phe Tyr Ile Asp
 595 600 605
 Phe Gly Gly Leu Lys Pro Ala Gly Ser Glu Pro Thr Pro Lys Ser Arg
 610 615 620
 20 Ile Ala Asp Leu Pro Pro Ala Asn Pro Asp His Ile Gly Gly Tyr Arg
 625 630 635 640
 Leu Ala Thr Ala Thr Phe Ala Gly Ile Glu Asn Lys Phe Gly Leu Tyr
 645 650 655
 Leu Pro Lys Phe Lys Ser Pro Ser Val Ala Val Val Gln Pro Lys Ala
 25 660 665 670
 Ala Val Ala Ala Thr Gln
 675

(2) INFORMATION FOR SEQ ID NO: 3:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

40

AAGCTTGGCA CGAGGCCTCG TGCCAAGGAG AACTTAGTTT CAGCAGCTGG AGGAAGTATC

60

	T C A C A C C A G G	T T A G C T T C T C	C T A C T T C A A T	G C A T T T A A C T	O G T T A C T G A A	T A A C A T G G A G	120
	C T T G T T C G T A	A G A T A T A T A G	C A C T C T A G C T	G G C A C A A G G A	A A G A T G T T G A	A G T C A C A A A G	180
	G A G G A A T T T G	C C C A G A G T G C	C A T A C G C T A T	G G A C A A G T C A	C A C C A C T A G A	A A T T G A T A T T	240
	C T A T A T C A G C	T T G C A G A C T T	A T A T A A T G C T	T C A G G G C G C T	T G A C T T T G G C	A G A T A T T G A G	300
5	A G A A T A G C C C	C A T T G G C T G A	G G G G G C C T T A	C C T T A C A A C C	T G G C A G A A C T	T C A G A G A C A G	360
	C A G T C T C C T G	G G T T A G G C A G	G C C T A T C T G G	C T C C A G A T T G	C C G A G T C T G C	T T A C A G A T T C	420
	A C T C T G G G K C	T C A G T T G C T G	G A G C T G T G G G	A G C C A C T G C A	G T G T A T C C T A	T A G A T C T G G T	480
	G A A G A C C C G A	A T G C A A A A C C	A G C G T G G C T C	T G G C T C T G T T	G T T G G G G A G C	T A A A T G T A C A	540
	A A A C A G C T T	T G A C T G T T T T	A A G A A A G T Y T	T G C G T T A T G A	G G G C T T T C T T	T G G A C T C T A C	600
10	A G G G G T C T G A	T A C C A C A A C T	T A T A G G G G T T	K C T C C A G A A A	A G G C C A T T A A	A C T G A C T G T T	660
	A A T G A T T T T G	T T C G G G A C A A	A T T T A C C A G A	A G A G A T G G C T	C T G T T C C A C T	T C C A G C A G A A	720
	G T T C T G C T G	G A G G C T G T G C	T G G A G G C T C T	C A G G T C A T T T	T T A C C A A C C C	A T T G G A G A T A	780
	G T G A A G A T T C	G T C T G C A A G T	A G C T G G A G A G	A T C A C C A C G G	G A C C C A G A G T	C A G C G C C C T G	840
	A A T G T G C T C C	G G G A C T T G G G	A A T T T T T G G T	C T G T A T A A G G	G T G C C A A A G C	G T G T T C C T C	900
15	C G A G A C A T T C	C C T T C T C T G C	A A T C T A T T T T	C C T G T T T A T G	C T C A T T G C A A	A C T A C T T C T G	960
	G C T G A T G A A A	A T G G A C A A C G	T G G G A G G T T T	A A A T C T T C T T	G C A G C T G G R A	G C C A T G G C A G	1020
	G T G T C C C A G C	T G C A T C T C T G	G T G G A M C C C Y	G C T G A T G T C A	T C A A R G A C A A	R G A C T G C A G G	1080
	T K G S T G C C C G	C G C T G G C C A G	A C G A C A T A C A	G T G G T G T C A T	C G A C T G T T T C	A G G A A G A T T C	1140
	T C C C G G G A A G	A A G G S C C T C A	G C A T T T T G G A	A A G G G A C T K C	A G C T C G A G T G	T T T C G A T C C T	1200
20	C T C C C C A G T T	T G G T G T T A C C	T T G G T C A C T T	A T G A A C T T C T	C C A G C G G T G G	T T T T A C A T T G	1260
	A T T T T G G A G G	C C T C A A A C C C	G C T G G T T T C A	G A A C C A A C A C	C T A A G T C A C G	C A T T G C A G A C	1320
	C T T C C T C C T G	C C A A C C C T G A	T C A C A T C G G T	G G A T A C A G A C	T C G C C A C A G C	C A C G T T T G C A	1380
	G G C A T C G A A A	A C A A A T T T G G	C C T T T A T C T C	C C G A A A T T T A	A G T C T C C T A G	T G T T G C T G T G	1440
	G T T C A G C C A A	A G G C A G C A G T	G G C A G C C A C T	C A G T G A T G A G	A C A A C T G T T G	G A G T G T G G C A	1500
25	A A A T G G G C C C	T T G A A G A A A G	A G G C C T A G G A	G A G C A G C C C T	G T A A T G T A T C	C A G T C A G C T G	1560
	C A T G G T A C T G	A C T G A G C T G A	G G A G T C A A A C	T C T T C T T T C T	G T A T G A C A T A	T A C A T A T A C T	1620
	T G T T T A T A A A	A T A A T C A T T T	G C C C A G G G A A	A A A C C A C A A	C G C T G T T T C A	A G C T T T A G T C	1680
	T T A T G T G T T G	A A A T G T T T T T	G T A A G C C T T G	G C A T G A A T T A	G T G T T C T A G A	C T C T G C T T T G	1740
	C A C A G C T T G C	A C T T A C A G T G	A T T G T A C A T A	T T G T A C A T C T	T T G T A C A G A G	A C A T C T T G G C	1800
30	A C C T C A T C C C	A A C A A T C A C	A T T T G T A G A A	A T G T A A T G C G	G T T C T G A G T G	G C T T G A A A T G	1860
	T A C A G A A T G T	T T T G A A A G T G	T T T T A T T A A G	A A T C A C A C A A	A A A T A A A T G T	A T T A A A A T T A	1920
	A A T T C A T T C T	C T T A T T G G T G	A C T T A T G G A A	A T A A A G C A T C	A A T A T T G G A T	G T A T T T A A T T	1980
	C C T A G T T K G T	T T T C C A T T C T	G G A A T A A A A A	G G T A T T T G C T	G A T A A A A G G C	A T A A C G A G A C	2040
	A T A G T G C T G C	T A C C A C T G A A	T A A G T G A T A C	T T T G G G A A A G	A T G C C A T G C C	A G T G G A T G C C	2100
35	A G A G G A C C A G	G C T A A T G A C T	T G T G T G T G C T	G A T G T G K T T T	C C A T T T G T A T	T T A A T G T G T G	2160
	T A G A C C C T C C	T C T G T T C A T C	A A T C A A A A A G	C A T T T C C T A G	G H A G C T C C T C	G C C T G T C A G T	2220
	G T G C A T A T G G	A A A C A G G G A C	A T C T C C A Y C A	T T A C T G G C T T	A G T T K K S Y T T	Y C Y T T T G A C A	2280
	C A G T A A G G C A	A A G G C C A A G C	T T T C A A A A G A	G T A A A G G A T A	C T T T C A C A A T	T T C C C T C A T	2340
40	A T G G A T A T G A	T T C C A G T C A A	A A A T A A A A T G	C A C A C C A A A A	T G T A A A A A A A	A A A	2393

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 453 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Glu Leu Val Arg Lys Ile Tyr Ser Thr Leu Ala Gly Thr Arg Lys
 1 5 10 15
 Asp Val Glu Val Thr Lys Glu Glu Phe Ala Gln Ser Ala Ile Arg Tyr
 15 20 25 30
 Gly Gln Val Thr Pro Leu Glu Ile Asp Ile Leu Tyr Gln Leu Ala Asp
 35 40 45
 Leu Tyr Asn Ala Ser Gly Arg Leu Thr Leu Ala Asp Ile Glu Arg Ile
 50 55 60
 Ala Pro Leu Ala Glu Gly Ala Leu Pro Tyr Asn Leu Ala Glu Leu Gln
 20 65 70 75 80
 Arg Gln Gln Ser Pro Gly Leu Gly Arg Pro Ile Trp Leu Gln Ile Ala
 85 90 95
 Glu Ser Ala Tyr Arg Phe Thr Leu Gly Leu Ser Cys Trp Ser Cys Gly
 25 100 105 110
 Ser His Cys Ser Val Ser Tyr Arg Ser Gly Glu Asp Pro Asn Ala Lys
 115 120 125
 Pro Ala Trp Leu Trp Leu Cys Cys Trp Gly Ala Lys Cys Thr Lys Thr
 130 135 140
 Ala Leu Thr Val Leu Arg Lys Xaa Cys Val Met Arg Ala Phe Phe Gly
 30 145 150 155 160
 Leu Tyr Arg Gly Leu Ile Pro Gln Leu Ile Gly Val Xaa Pro Glu Lys
 165 170 175
 Ala Ile Lys Leu Thr Val Asn Asp Phe Val Arg Asp Lys Phe Thr Arg
 35 180 185 190
 Arg Asp Gly Ser Val Pro Leu Pro Ala Glu Val Leu Ala Gly Gly Cys
 195 200 205
 Ala Gly Gly Ser Gln Val Ile Phe Thr Asn Pro Leu Glu Ile Val Lys
 210 215 220
 Ile Arg Leu Gln Val Ala Gly Glu Ile Thr Thr Gly Pro Arg Val Ser
 40 225 230 235 240

32

Claims

1. An isolated polypeptide comprising an amino acid sequence which has at least 70% identity to the amino acid sequence of SEQ ID NO:2 over the entire length of of SEQ ID NO:2.
- 5 2. An isolated polypeptide as claimed in claim 1 in which the amino acid sequence has at least 95% identity.
3. The polypeptide as claimed in claim 1 comprising the amino acid sequence of SEQ ID NO:2.
- 10 4. The isolated polypeptide of SEQ ID NO:2.
5. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide that has at least 70% identity to the amino acid sequence of SEQ ID NO:2, over the entire length of SEQ ID
- 15 NO:2; or a nucleotide sequence complementary to said isolated polynucleotide.
6. An isolated polynucleotide comprising a nucleotide sequence that has at least 70% identity to a nucleotide sequence encoding a polypeptide of SEQ ID NO:2, over the entire coding region; or a nucleotide sequence complementary to said isolated polynucleotide.
- 20 7. An isolated polynucleotide which comprises a nucleotide sequence which has at least 70% identity to that of SEQ ID NO:1 over the entire length of SEQ ID NO:1; or a nucleotide sequence complementary to said isolated polynucleotide.
- 25 8. The isolated polynucleotide as claimed in any one of claims 5 to 7 in which the identity is at least 95%.
9. An isolated polynucleotide selected from:
 - (a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO:2;
 - 30 (b) the polynucleotide of SEQ ID NO:1; and
 - (c) a polynucleotide obtainable by screening an appropriate library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO:1 or a fragment thereof; or a nucleotide sequence complementary to said isolated polynucleotide

10. An expression system comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression system is present in a compatible host cell.
11. A host cell comprising the expression system of claim 10 or a membrane thereof expressing the polypeptide of claim 1.
12. A process for producing a polypeptide of claim 1 comprising culturing a host cell of claim 11 under conditions sufficient for the production of said polypeptide and recovering the polypeptide from the culture medium.
13. An antibody immunospecific for the polypeptide of claim 1.
14. A method for screening to identify compounds which stimulate or which inhibit the function of the polypeptide of claim 1 which comprises a method selected from the group consisting of:
- (a) measuring the binding of a candidate compound to the polypeptide (or to the cells or membranes bearing the polypeptide) or a fusion protein thereof by means of a label directly or indirectly associated with the candidate compound;
- (b) measuring the binding of a candidate compound to the polypeptide (or to the cells or membranes bearing the polypeptide) or a fusion protein thereof in the presense of a labeled competitor;
- (c) testing whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells or cell membranes bearing the polypeptide;
- (d) mixing a candidate compound with a solution containing a polypeptide of claim 1, to form a mixture, measuring activity of the polypeptide in the mixture, and comparing the activity of the mixture to a standard; or
- (e) detecting the effect of a candidate compound on the production of mRNA encoding said polypeptide and said polypeptide in cells, using for instance, an ELISA assay.
15. An agonist or antagonist to the polypeptide of claims 1 to 4.
16. A compound which is:
- (a) an agonist or antagonist to the polypeptide of claims 1 to 4;
- (b) isolated polynucleotide of claims 5 to 9; or

- (c) a nucleic acid molecule that modulates the expression of the nucleotide sequence encoding the polypeptide of claim 1;
for use in therapy.
- 5 17. A process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the polypeptide of claim 1 in a subject comprising:
- (a) determining the presence or absence of a mutation in the nucleotide sequence encoding said polypeptide in the genome of said subject; and/or
- (b) analyzing for the presence or amount of said polypeptide expression in a sample derived
10 from said subject.
18. An isolated polynucleotide selected from the group consisting of:
- (a) an isolated polynucleotide comprising a nucleotide sequence which has at least 70% identity to SEQ ID NO:3 over the entire length of SEQ ID NO:3;
- 15 (b) an isolated polynucleotide comprising a nucleotide sequence which has at least 70% identity to SEQ ID NO:1 over the entire length of SEQ ID NO:3;
- (c) an isolated polynucleotide comprising the polynucleotide of SEQ ID NO:3;
- (d) the polynucleotide of SEQ ID NO:3; or
- (e) an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide which has
20 at least 70% identity to the amino acid sequence of SEQ ID NO:4, over the entire length of SEQ ID NO:4.
19. A polypeptide selected from the group consisting of:
- (a) a polypeptide which comprises an amino acid sequence which has at least 70% identity to
25 that of SEQ ID NO:4 over the entire length of SEQ ID NO:4;
- (b) a polypeptide in which the amino acid sequence has at least 70% identity to the amino acid sequence of SEQ ID NO:4 over the entire length of SEQ ID NO:4;
- (c) a polypeptide which comprises the amino acid of SEQ ID NO:4;
- (d) a polypeptide which is the polypeptide of SEQ ID NO:4;
- 30 (e) a polypeptide which is encoded by a polynucleotide comprising the sequence contained in SEQ ID NO:3.

INTERNATIONAL SEARCH REPORT

national Application No
PCT/EP 98/05115

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/47 C07K16/18 G01N1/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	DATABASE EMBL (TREMBL), 01 JAN 1998, accession no. 014566, GOELA D. and HULTMAN M.: "human BAC clone GS244B22; similarity: belongs to the mitochondrial carrier family". XP002089570 see abstract	1-19
A	DATABASE EMBL, 01 NOV 1996, accession number Q21153, WILSON R. et al.: "K02F3.2, Caenorhabditis elegans, similarity: belongs to the mitochondrial carrier family." XP002089571 see abstract	1-19

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

11 January 1999

Date of mailing of the international search report

29. 01. 99

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Hardon, E

INTERNATIONAL SEARCH REPORT

I national Application No

PCT/EP 98/05115

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>SHINOHARA Y ET AL: "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator." BIOCHIMICA ET BIOPHYSICA ACTA, (1993 OCT 10) 1152 (1) 192-6. JOURNAL CODE: AOW. ISSN: 0006-3002., XP002089540 Netherlands see the whole document ---</p>	1-19
A	<p>SCHIEBEL K ET AL: "A human pseudoautosomal gene, ADP/ATP translocase, escapes X-inactivation whereas a homologue on Xq is subject to X-inactivation." NATURE GENETICS, (1993 JAN) 3 (1) 82-7. JOURNAL CODE: BRO. ISSN: 1061-4036., XP002089541 United States see the whole document ---</p>	1-19
A	<p>WALKER J E ET AL: "The mitochondrial transport protein superfamily." JOURNAL OF BIOENERGETICS AND BIOMEMBRANES, (1993 OCT) 25 (5) 435-46. REF: 50 JOURNAL CODE: HIO. ISSN: 0145-479X., XP002089542 United States see the whole document ---</p>	1-19
A	<p>KUAN J ET AL: "The mitochondrial carrier family of transport proteins: structural, functional, and evolutionary relationships." CRITICAL REVIEWS IN BIOCHEMISTRY AND MOLECULAR BIOLOGY, (1993) 28 (3) 209-33. REF: 80 JOURNAL CODE: DTM. ISSN: 1040-9238., XP002089543 United States see the whole document -----</p>	1-19

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 98/05115

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 6, 15 and 16 (partially)
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Claims Nos.: 6, 15 and 16 (partially)

1. Claim 6 defines a polynucleotide as comprising a nucleotide sequence that has at least 70% identity to a nucleotid sequence encoding a polypeptide of defined amino acid sequence. Back-translation of a polypeptide in DNA generates a very great number of nucleic acid sequences (of the order of 10^{47} for 100 amino acids). A comparison of an entire sequence database with all these hypothetical nucleic acids is not possible. The search thus has been limited to the conventional protein/protein and protein/six-frame translated nucleic acid comparisons.

2. Claims 15 and 16 define a group of products solely in functional terms, i.e. as agonist or antagonist to the polypeptide of the proceeding claims. A patent search can only recover the few (if any) products for which this function has been tested. This does not mean that other known products do not have this function. For claims which define agonists/antagonists solely in functional terms the search is thus necessarily incomplete.